

Figure 1A

## Figure 1B

Gal specific positives

E: 65 colonies  
X: 29 colonies



Repeat of screen with aniti-PTyr

E: 9 colonies  
X: 2 colonies



Rescue plasmid DNA



Retransformation into a yeast strain not expressing FGFR



Is activation of P-Tyr by plasmid FGFR dependent?

FGFR dependent P-Tyr: E: 8 genes , X: 2 genes

FGFR independent P-Tyr: E: 1 gene, X: 0

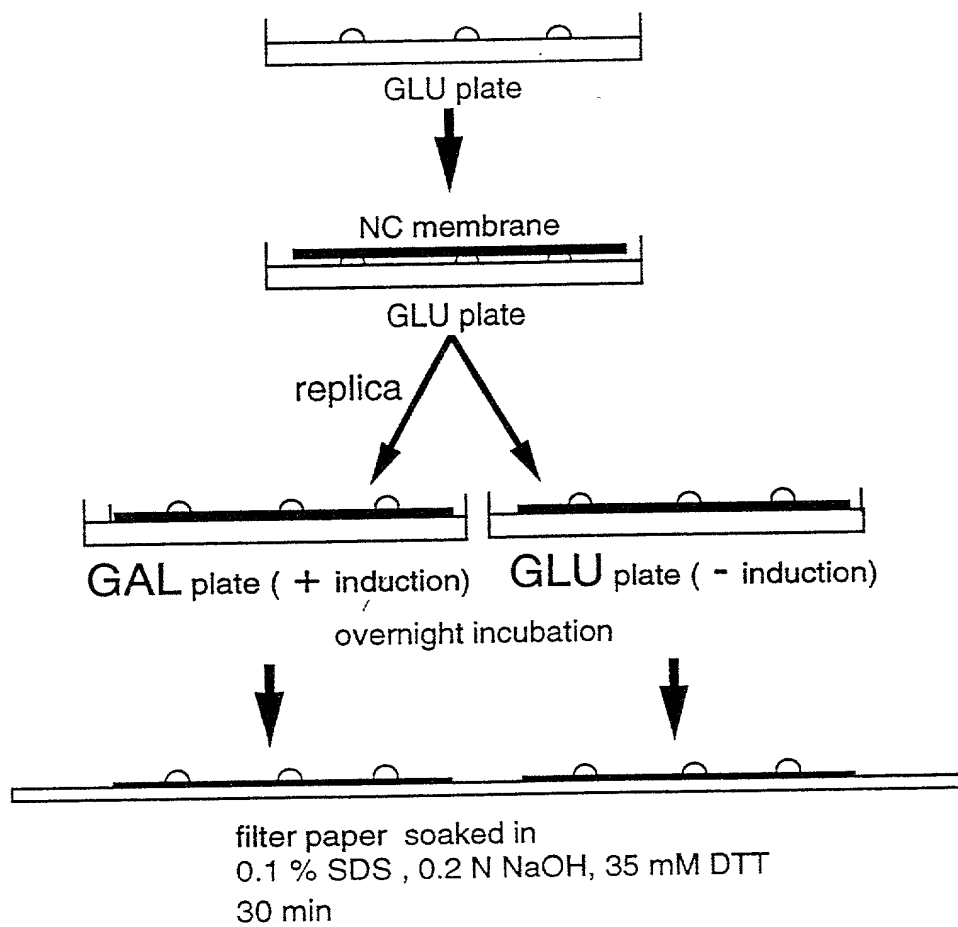


Figure 2

ALP cDNA  
ACCAAAAGAA CGACAGAACG AAGGAAAGAC AGAGACAGTC CTTGTTTTAA GACTCCAGGG 60  
GAATTTACGT CTAATAAAGA GAAGAGAGGC ATTGTATGCT TGACATTATG GTGGCAGTTT 120  
TATCTTCTCT GTTGACAATT TGCATTATCC TCAGCTTTTC TCTCCCATCC GATACCCAGA 180  
ATATCAATGC CTTTATGGAA AAGCACATTG TTAAGGAAGG AGCTGAAACA AACTGCAACC 240  
AAACCATCAA AGACAGAAAC ATCCGGTTTA AAAACAAC TG CAAATTCCGC AACACCTTTA 300  
TTCATGATAC CAATGGTAAA AAGGTGAAGG AGATGTGCGC TGGGATTGTC AAATCTACCT 360  
TTGTGATCAG CAAGGAACTG CTGCCTCTCA CTGACTGCTT GTTGATGGGA CGTACTGCAA 420  
GACCCCCAAA TTGTGCTTAT AATCAAACAA GAACAAC TG GGTCAATTAAT ATCACTTGTG 480  
AAAACAATTA CCCTGTGCAC TTTGCTGGGT ACAAATCAAG CTTCTGTGCT TCATATTCTC 540  
CATGTGCCTT AATAGTAATA ACTGTTTTCC TGCTCAGCCA GCTACTGCTC CCTGCTATGA 600  
GATGATGCCC AGAAACGGGA GTATCAATAG CTAAACTAG AAGGACTGAT AGTGATGGAT 660  
GATTGTTCTT AAGTCATTTA GAGATCTACC TGTGTTCACT TCCAAACAAA GAAGACATAG 720  
GTATAATTGA ATCAACCGTG ACATAGACTG ACTTCTAAAT AATAAAAGCA ACATTTTCTG 780  
TTTTAACAAA AAAAAAAAAA AAAAAAAAAA 809

Figure 3

ALP  
MLDIMVAVLSLLTICIILSFSLPSDTQNINAFMEKHIV  
KEGAETNCNQTIKDRNIRFKNNCKFRNTFIHDTNGKKVK  
EMCAGIVKSTFVISKELLPLTDCLLMGRTARPPNCAYNQ  
TRTTGVINITCENNYPVHFAGYKSSFCASYSPCALIVIT  
VFLLSQLLLPAMR

Figure 4

1001644-121001

FOOTPRINT CHART

MLDIMVAVLSLLTICILSFSLPSDTQININAFMEKHIVKEGAETN---CNQTIKDRNIRFKNN  
 AQDDYRYIHFLTQHYDAKPKGRNDE-YCFNMMKNRRTRP---  
 VQPSLGKESAAMK FERQHMDSTVATSSSPTYCNQMMKRRNMTQGQE

CKDRNTFIHG NKNDIKAICEDRN-GQPYRGDLRI-SKSEFQITICKHKGSSRPP-CRYGATED-  
 CKFRNTFIHDTNGKKVKEMCAGI-VKSTFVISKEL-----LPLTDCLLMGRTARPPNCAYNQTRT-  
 CKPVNTFVHESLAD-VHAVCSQENVKCKNGKSNKYKSHSALHITBCRLKGNKAKYP-NC DY-QTSQH

SRVIVVGCENG--LPVHFDESFITRPH  
 TGVINITCENN--YPVHFAGYKSSFCASYSPCALIVITVFLLSQLLLPAMR  
 QKHIIIVACEGNPFVPVHFDATV

bovine angiogenin (28.8%)

Xenopus ALP

Chinese Hamster pancreatic RNase (32.3%)

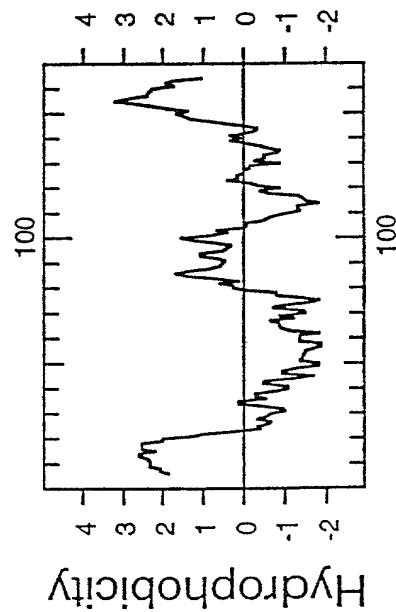


Figure 5

CLP cDNA  
ATTTACCACC GACCGTTACA CCTGGTTTTT GCTAAGGACA CATTCAATAC AAGAACTAAA 60  
AGTGGGAAAC TGGGGCCTTT GCAGAAAACA ATGCAGTTTT TAAGATTTCT TGCCATCCTT 120  
ATTTTCTCTG CTAAACATTT TATCAAGCAT TGCAAAGGTG AACTTGCAT GGGACTGAAC 180  
TGTAATGACC CAAGGTTATT GGAGGCAATT AAGAGCAACA CAATCAATCA GCTCTTGCAT 240  
GATACAATTA ATGCCACCCA TGGAAAGAGT CCACCAAAAT CCACTAAAAC CTTGCCCTTC 300  
TTGGGTATCA CAGACAGTAA GAAATTGAAT AGAAAATGCT GTCAGAATGG AGGCACTTGT 360  
TTCTTGGGGA CCTTTTGCAT CTGCCCTAAG CAATTTACTG GTCGGCACTG TGAACATGAA 420  
AGGAGGCCAG CAAGCTGCTC CGGTGTTCCC CATGGAGACT GGATCCGTCA GGGCTGCTTG 480  
CTGTGTAGAT GTGTGTCTGG TGTCTTACAC TGCTTCAAGC CCGAGTCTGA GGACTGTGAT 540  
GTTGTGCATG AAAAAACAT GAGATCGGGG GTCCCAGAA TGCAGCTCAG CTTAATCATC 600  
TATTGCTTCC TTACTGCAAA CTGTGTTTAC CACATAGTTT GGCATCTGAA TATTGGACTT 660  
TAACAGAGTA ACTTGAGTCT GCCAGTCAGG TTCAGATTGC AGACGTCTGT GTCTACACTG 720  
CACTTTCAAT TTGTGAACCC ATTTTGCCAG GATTATGCTT GAAGTATATG GCTATCTTCC 780  
ACCCCTGGAA TCCTGGAAAA TATGCAGAAA CTATACAATG CCTTATTTCT ATTGGTTGTT 840  
TCATAAAATA ACTTTTTTTT TAGGATGATG TGTATAGTGG CCAGAATGGG TTTACAGTAC 900  
TTCCAAGCAC TGGCGTTGGT TCAAATAGC TACTGGGTTT TTGCTCTTTG CTGCATGTTG 960  
AGATCAGGAA GCTAGTCTTA TACTTACCCA GTGCATTCTG TATATATGTA AATTTTATTA 1020  
ACTTATTAGA CACGTTGTAC ATTAACAGCA TCCTTCACAA ACTTTTATTT TTTTAAATT 1080  
TTTTTATTAA TTGACAAAGA GAACAAAGTA TCTAGGAACA TTTTACAAAT ATTGTCCTAC 1140  
TACATTGCAT GTTGTGGTTC TTGTTTGTAT GTTGTCTCTG ATCTTCTACA ATGTATCCCT 1200  
AGCCATAAAA CGATTTTGTG AGTGTGTGTG TGTGACTGCA TCCCATTTTA TTCATTATGC 1260  
AAACACTTTG CAAATGATTG TGCAGCAATG TAAGTGCTAG CCTGTGGTCA ACAGTGCTGA 1320  
ATGTAAATCT TGGAGCGGTG ATATCAGCAT GCTTATGGAG GCTCAATAAC CTTGGTCTTG 1380  
CCCCTTTAAA TTCTATTTTT CTACGGGCAA GTAAATCTAA ACTGGTAAAG TACCTTCTTT 1440  
TAAGGAAATG AATCACTGAA TGTATAATT CCAGTTTCAG GCCACAGACA ATTAATGACA 1500  
GCTCAGGGAA TAATACAATT GCCCATGTTT GATGCACCTA ATGTAAGTGA TGTATTACAG 1560  
GGTGTCTGCT TGATGTTTGC AATGAAGACA TTAAATACTG TACCTAAAAG AAAAAAAAAA 1620  
AAAAAAAAA AAA 1633

Figure 6

CLP  
MQFLRFLAILIFSAKHFIKHCKGETCMGLNCNDPRLLEA  
IKSNTINQLLHDTINATHGKSPPKSTKTLPLFLGITDSKK  
LNRKCCQNGGTCFLGTFCICPKQFTGRHCEHERRPASCS  
GVPHGDWIRQGCLLCRCVSGVLHCFKPESEDCDVVHEKN  
MRSGVPRMQLSLIIYCFLTANLFYHIVWHLNIGL

Figure 7

4001644-131001



1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
18	18	18	18
19	19	19	19
20	20	20	20
21	21	21	21
22	22	22	22
23	23	23	23
24	24	24	24
25	25	25	25
26	26	26	26
27	27	27	27
28	28	28	28
29	29	29	29
30	30	30	30
31	31	31	31
32	32	32	32
33	33	33	33
34	34	34	34
35	35	35	35
36	36	36	36
37	37	37	37
38	38	38	38
39	39	39	39
40	40	40	40
41	41	41	41
42	42	42	42
43	43	43	43
44	44	44	44
45	45	45	45
46	46	46	46
47	47	47	47
48	48	48	48
49	49	49	49
50	50	50	50
51	51	51	51
52	52	52	52
53	53	53	53
54	54	54	54
55	55	55	55
56	56	56	56
57	57	57	57
58	58	58	58
59	59	59	59
60	60	60	60
61	61	61	61
62	62	62	62
63	63	63	63
64	64	64	64
65	65	65	65
66	66	66	66
67	67	67	67
68	68	68	68
69	69	69	69
70	70	70	70
71	71	71	71
72	72	72	72
73	73	73	73
74	74	74	74
75	75	75	75
76	76	76	76
77	77	77	77
78	78	78	78
79	79	79	79
80	80	80	80
81	81	81	81
82	82	82	82
83	83	83	83
84	84	84	84
85	85	85	85
86	86	86	86
87	87	87	87
88	88	88	88
89	89	89	89
90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

MQFLRFLAILFSAKHFIKHCKGETCMGLNCNDPRLLAEIKSNTINQLLHDTINATHGKSPF  
MGYFSSSVLLVAISSAFEFPGPVAGRDLAIRDNSIWDQKEPAVRD

\* \* \* \* \*

KSTKTLPLGITDSKKLNRRKCCQNGGTCFLGTFCICPKQFTGRHCEHERRPASC SGVPHGDWIRQGCLLCRCVSGVLHCF  
RSFQFVPVGVIQNSKSLSNKTCCLNGGTCILGSFCACPPSFYGRNCEHDVRKEHGCSILHGTWL P KKC SLCRCWHGQLHCL

KPESEDCDVVHEKNMRSGVPRMQLSLIICYFLTANLFYHIVWHLNIGL  
PQTELPGCDGHVMDQDLKASRTPCQTPSVTTTFML

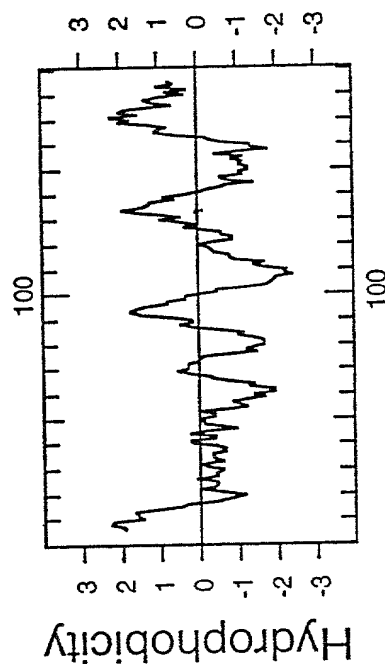


Figure 8

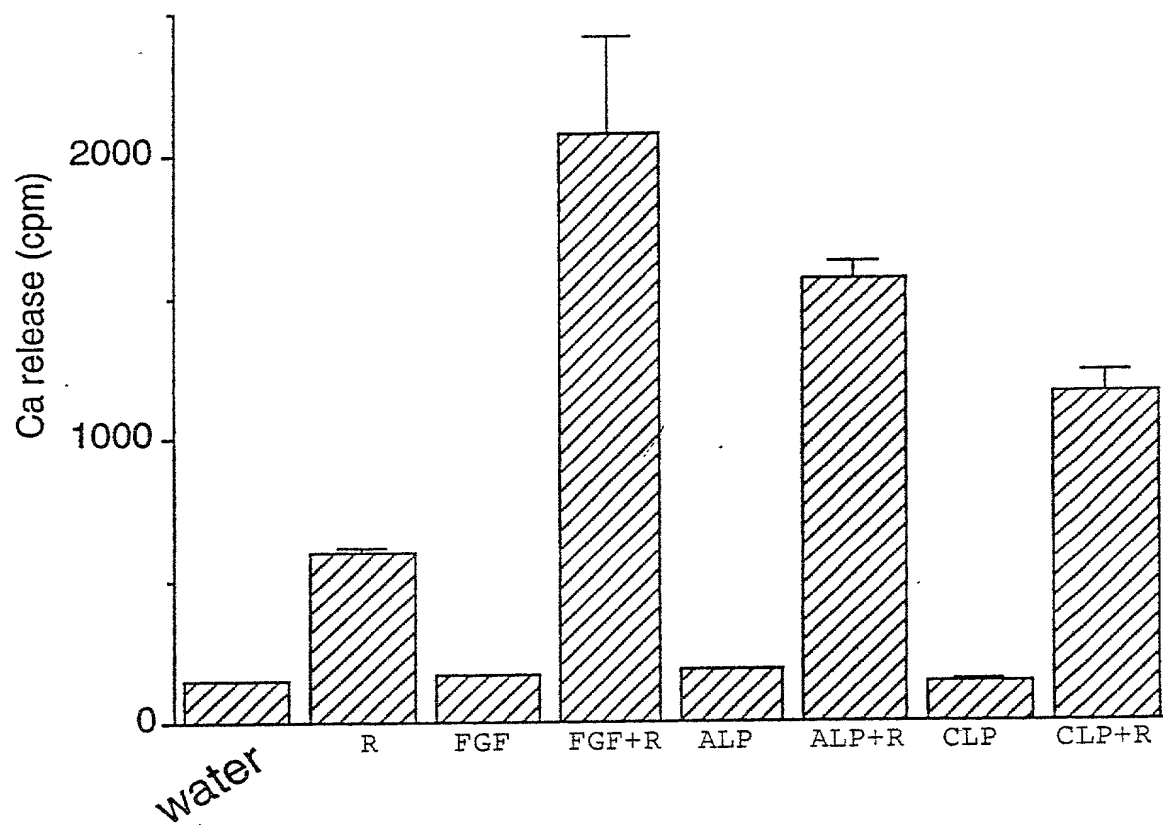
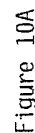


Figure 9



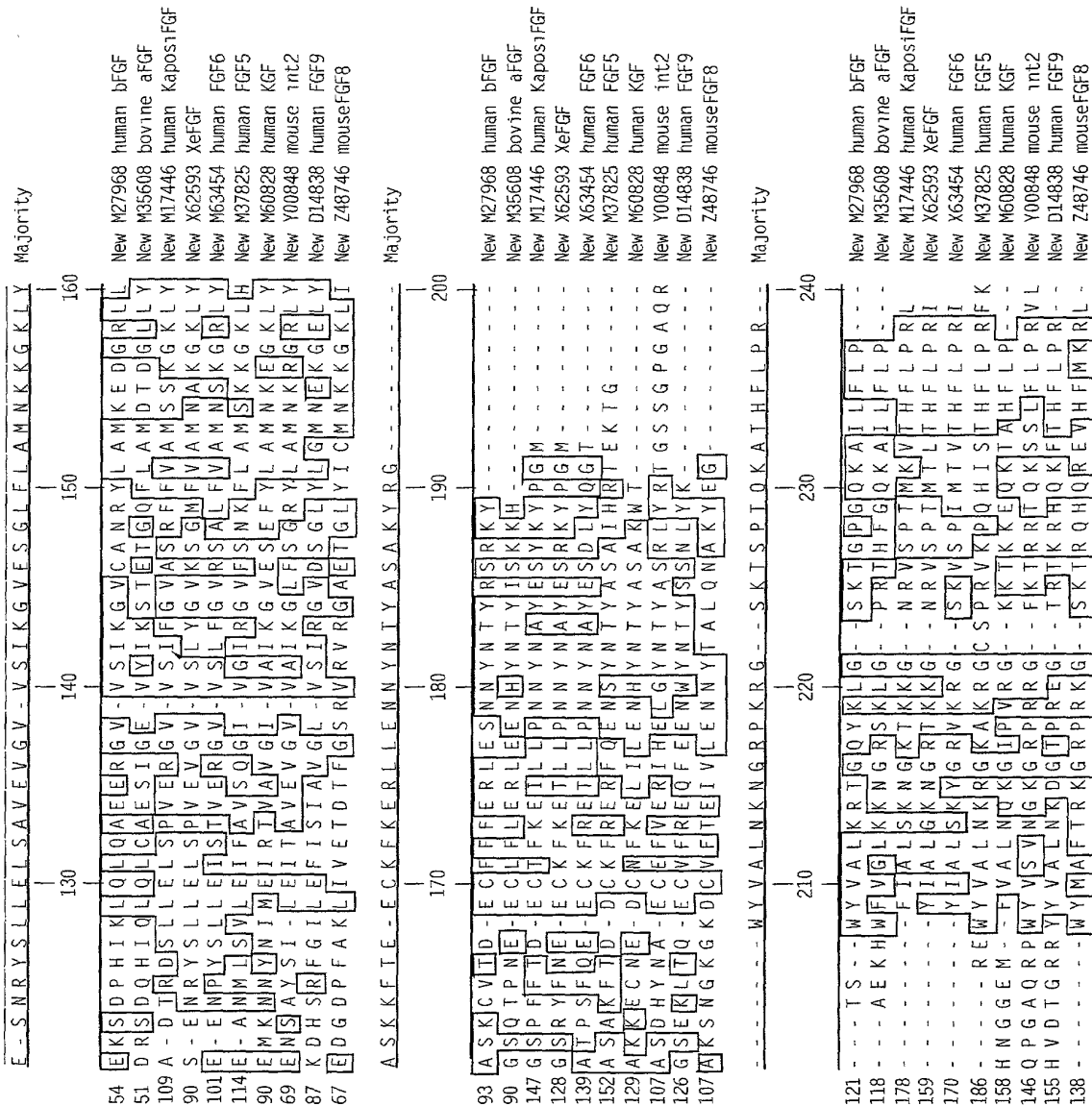


Figure 108

(CLP) ↓  
MQFLRFLAILIFSAKHFIKHCKGETCMGLNCNDPRLLLEAI 40  
KSNTINQLLHDTINATHGKSPPKSTKTLPLGITDSKKLN 80  
RKCCQNGGTCFLGTFCICPKQFTGRHCEHERRPASCSGVP 120  
HGDWIROGCLLCRCVSGVLHCFKPESEDCDVVHEKNMRSG 160  
VPRMQLSLIIYCFLTANLFYHIVWHLNIGL 190

(ALP) ↓  
MLDIMVAVLSSLLTICIIILSFSLPSTQNINAFMEKHIVK 40  
EGAETNCNQTIKDRNIRFKNNCKFRNTFIHDTNGKKVKEM 80  
CAGIVKSTFVISKELLPLTDCLLMGRTARPPNCAYNQTRT 120  
TGVINITCENNYPVHFAGYKSSFCASYSPCALIVITVFL 160  
SQLLLPAMR 169

arrow; predicted cleavage sites  
N: predicted N-glycosylation sites

Hydrophobic regions at C-terminus are underlined

Figure 11

10016447-121001

FRL-1  
MQFLRFLAILIFSAKHF IKHCKGETCMGLNCNDPRLLEA

IKSNTINQLLHDTINATHGKSPPKSTKTL PFLGITDSKK

\*   \*   \*   \*   \*   \*  
LNRKCCQNGGTCFLGTFCICPKQFTGRHCEHERRPASCS

\*   \*   \*  
GVPHGDWIRQGCLLCRCVSGVLHCFKPESEDCDVVHEKN

MRSGVPRMQLSLIIYCFLTANLFYHIVWHLNIGL

\*: amino acid residues highly conserved among EGF  
repeats

Figure 12

10016447-121001